

is preferably in substantial isolation from other polypeptides of plant origin, and more preferably in substantial isolation from any other polypeptides. The polypeptide may have amino acid residues NSKH (SEQ ID NO: 32) at about position 697 (in the sequence shown in Figure 4 (SEQ. ID. NO. 29)), instead of the sequence DA D/E Y (SEQ ID NO: 33) found in other SBE class A polypeptides. The polypeptide may be used in a method of modifying starch *in vitro*, the method comprising treating starch under suitable conditions (of temperature, pH etc.) with an effective amount of the polypeptide.

Please replace the paragraph beginning on page 17, line 19 with the following paragraph:

To confirm this a primer (CSBE218, SEQ. ID. NO. 19) was made to a region in the 3' UTR (untranslated region) of pSJ101 and used in combination with CSBE214 (SEQ. ID. NO. 15) primer to recover by PCR a full length cDNA from both leaf and root cDNA. These clones were sequenced and designated pSJ106 & pSJ107 respectively. The sequence and predicted ORF of pSJ107 is shown in Figure 4 (SEQ. ID. NO. 28). The long ORF in plasmid pSJ106 was found to be interrupted by a stop codon (presumably introduced in the PCR process) approximately 1 kb from the 3' end of the gene, therefore another cDNA clone (designated pSJ116) was amplified in a separate reaction, cloned and sequenced. This clone had an intact ORF (data not shown).

There were only a few differences in these two sequences (in the transit peptide aa 27-41: YRRTSSCLSFNFKEA (SEQ ID NO: 34) to DRRTSSCLSFIFKAA (SEQ ID NO: 35) and L831 in pSJ107 to V in pSJ116 respectively).

Please replace the paragraph beginning on page 19, line 17 with the following paragraph:

A comparison of all known SBE II protein sequences shows that the cassava SBE II gene is most closely related to the pea gene (Figure 8). The two proteins are 86.3% identical over a 686 amino acid range which extends from the triple proline "elbow" (Burton *et al.*, 1995 Plant J. 7, 3-15) to the conserved VVYA (SEQ ID NO: 36) sequence immediately preceding the C-terminal extensions (data not shown). All SBE II proteins are conserved over this range in that they are at least 80% similar to each other. Remarkably however, the sequence conservation

between the pea, potato and cassava SBE II proteins also extends to the N-terminal transit peptide, especially the first 12 amino acids of the precursor protein and the region surrounding the mature terminus of the pea protein (AKFSRDS (SEQ ID NO: 37)). Because the proteins are so similar around this region it can be predicted that the mature terminus of the cassava SBE II protein is likely to be GKSSHES (SEQ ID NO: 38). The precursor has a predicted molecular mass of 96 kD and the mature protein a predicted molecule mass of 91.3 kD. The cassava SBE II has a short acidic tail at the C-terminal although this is not as long or as acidic as that found in the pea or potato proteins. The significance of this acidic tail, if any, remains to be determined. One notable difference between the amino acid sequence of cassava SBE II and all other SBE II proteins is the presence of the sequence NSKH (SEQ ID NO: 32) at around position 697 instead of the conserved sequence DAD/EY (SEQ ID NO: 33). Although this conserved region forms part of a predicted α -helix (number 8) of the catalytic $(\beta/\alpha)_8$ barrel domain (Burton et al 1995 cited previously), this difference does not abolish the SBE activity of the cassava protein as this gene can still complement the glycogen branching deletion mutant of *E. coli*. It may however affect the specificity of the protein. An interesting point is that the other cassava SBE II clone pSJ94 has the conserved sequence DADY.

Please delete the previous sequence listing and substitute therefore new pages 1-24 which comprise the paper copy of the corrected Sequence Listing and renumber them accordingly.

In the claims:

Please cancel claims 1-11, 16-27 and 32.

Please add the following new claims:

33. An isolated nucleic acid from cassava, wherein the isolated nucleic acid encodes a polypeptide having starch branching enzyme Class A (SBEII) activity.
34. An isolated nucleic acid according to claim 33, and its complement, wherein the isolated nucleic acid has at least 88% sequence identity to SEQ ID NO: 28.